Microarray Repository SIG Meeting Minutes

Date, Time & Location:	July 7, 2004, 2004 2:00 – 3:00 EDT
Attendees:	Jomol Mathew– NYU Kuo-Tung Li - UC Irvine Paul Spellman – Lawrence Berkeley Lab Leo Cheung – U of Hawaii Michael Reich – MIT Jennifer Shoemaker – Duke Mervi Heiskanen – NCI Subha Madhavan – NCI Claire Zhu – BAH Juli Klemm - BAH

Review Discussions:	**Review discussion of last meeting (5/5/04)**
	
	- Group discussed the storage of data as "BLOBS" or flat-files to enable the data to be readily passed to other analysis tools. Storing the data relationally can enable powerful queries
	- The group discussed the importance of using the MIAME standard for capturing microarray data and the challenges this entails.
	- Data quality descriptors for microarray data sets were identified as important in order to ensure confidence in data analysis.
	
	Review of Developer/Adopter activities
	
	caArray: Currently slated for funded caArray adoption are NYU and Georgetown. UC San Francisco and The Burnham Institute will be adopting caArray as part of their Developer activities.
	
	- caArray user acceptance testing (Mervi Heiskanen)
	
	    o Scheduled for mid-August
	
	    o A good opportunity for interested parties to test usage of caArray.
	
	    o Test plan and training materials will be provided to participants 2 weeks before the testing. Application support always available.
	
	    o An email will be sent to this SIG soliciting participation in this user acceptance testing
	
	Microarray data sharing: Thomas Jefferson has a core facility supporting microarray data repository for the zebrafish consortium. They will be sharing out this data repository to Adopters (Sloan), and ultimately to the caBIG community.
	
	Future Activities
	
	- In the future, this meeting will be used to update on ongoing project activities.
	- Set standards for data sharing for consumers and producers of microarray data in caBIG.
	
	    o caArray API
	
	    o MAGE-ML
	
	        ▪ Key is agreeing on semantic meaning of column headers. Example: For GenePix, only 8 of the column headers readily map

to MAGE-ML. The rest are specialized data.

- Standard Affymetrix files are easily mapped to MAGE-ML, more complicated when producing derived data tables.

- Resulting files are very large and therefore can be tricky to manage.

Review of Mission Statement

- The purpose of the mission statement is to identify needs and opportunities and to facilitate communications within and outside the caBIG community.

- Comments/suggestions

    o Interoperability should be added to ensure that tools and data relevant to microarray repository are truly interoperable within this SIG. (Juli)

    o This SIG should work closely with V&CDE Workspace to ensure implementation of appropriate standards. (Juli)

- Mission statements will be posted on the caBIG website when the new site is up.

Other Items Discussed	- Let Mervi or Juli know if interested in participating in the caArray user acceptance testing. - The face-to-face meeting is tentatively scheduled for August 24 and 25.

Action Items:	Name Responsible	Action Item	Date Due	Notes
	Juli Klemm	Revise and distribute Mission Statement	7/12/04	
	Juli Klemm/Mervi Heiskanen	Send solicitation email for caArray testing	7/12/04	
	Juli Klemm	Distribute meeting minutes	7/12/04	